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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/724,108	12/01/2003	Hideki Thoda	245694US0CONT	3217

22850 7590 07/16/2007

OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
1940 DUKE STREET
ALEXANDRIA, VA 22314

EXAMINER	
SCHLAPKOHL, WALTER	

ART UNIT	PAPER NUMBER
1636	

NOTIFICATION DATE	DELIVERY MODE
07/16/2007	ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

patentdocket@oblon.com
oblonpat@oblon.com
jgardner@oblon.com

Office Action Summary	Application No.	Applicant(s)	
	10/724,108	THODA ET AL.	
	Examiner	Art Unit	
	Walter Schlapkohl	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *16 April 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *14-25* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *14-25* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☒ Other: *Exhibit B*.

DETAILED ACTION

Receipt is acknowledged of the papers filed 4/16/2007 in which claims 14 and 20 were amended. Claims 14-25 are pending and under examination in the instant Office action.

Continued Examination Under 37 CFR 1.114

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 4/16/2007 has been entered.

Specification/Application Data Sheet

The objection to the specification and to the ADS are hereby WITHDRAWN in view of Applicant's amendment filed 4/16/2007 and submission of a substitute ADS on 2/15/2007.

Claim Objections

Claims 15, 17, 21 and 23 are objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. The indicated claims broaden the scope of the independent claim from which they depend in that the independent claims are limited to either a pyruvate decarboxylase pdc1 enzyme and/or a serine protease isp6 enzyme and do not encompass any pyruvate decarboxylase as recited in claims 15 and 21, or any serine protease as recited in claims 17 and 23.

Claims 14 and 20 are objected to because of the following informalities: claims 14 and 20 each recite a list of enzymes wherein carboxypeptidase and zinc protease are listed twice (see, e.g., lines 5-6 of claim 14).

Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

The rejection of claim 20 under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention is hereby WITHDRAWN in view of Applicant's amendment.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 14-25 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the

claimed invention. **This rejection is maintained for reasons of record.**

Response to Arguments

Applicant argues that the rejection of the claims under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement is no longer applicable as the claims have been amended to define the genes listed in the Examples on pages 10-21. Applicant further argues that these genes were known in the art as evidenced by the references for the genes in the Examples ("SPC," "SPAC" etc) and as open reading frames from the genome sequence of *S. pombe* reported in the journal *Nature* **415**(6874):871-880, 2002. Applicant further argues that the fact that these gene structures were known indicates that the specification and claims satisfy the written description requirement.

Applicant's arguments have been carefully considered and have respectfully been found unpersuasive. Despite the fact that Applicant has amended the claims to define the "genes" listed in the examples present in the specification, the recited claims are still drawn to classes of enzymes which comprise numerous species. For example, among the "genes" listed by Applicant in claim 14 is "aminopeptidase" (see claim 14 at line

7). As is evidenced by Applicant's own specification, there are at least three different aminopeptideases from *S. pombe* which fall into such an enzyme class: dipeptidyl aminopeptidase, cytoplasmic aminopeptidase and aminopeptidase 1 (see specification at page 12, line 6; and page 16, lines 11-21). Indeed, a search in PubMed revealed 17 entries under "S. pombe aminopeptidase" with different sequences and therefore different biochemical properties (see Exhibit B, attached). Although it is clear that Applicant was in possession of sequence information for at least some of the genes encompassed by the claims, Applicant's reference to the *Nature* paper by Wood et al (*Nature* **415**(6874):871-880, 2002) is not persuasive because this paper was filed after Applicant's claimed priority date. Finally, the fact that some of the gene sequences encompassed by the claims were known at the time of Applicant's filing is not necessarily sufficient written description support for methods which require that such sequences be deleted in order to achieve increased production of a heterologous protein. In other words, Applicant has still not described a representative set of such sequences in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, was in possession of the claimed genus of sequences and sequence combinations capable of being deleted

such that production of any heterologous protein production was increased.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless -
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 14, 16, 20 and 22 are rejected under 35 U.S.C. 102(b) as being anticipated by Egel-Matani et al (US Patent No. 6,110,703; of record). **This rejection is maintained for reasons of record.**

Response to Arguments

Applicant argues that while Egel-Matini et al describe an *S. cerevisiae* YAP3, there is no disclosure for an *S. pombe* YAP3-type protease and certainly not the specific aspartic protease SPCC1795.09 as described in the specification and listed in the claims.

Applicant's arguments have been carefully considered and have respectfully been found unpersuasive. Egel-Matani et al do

in fact teach a YAP3 enzyme from *S. pombe* at columns 19-20, claims 1 and 11. With regard to Applicant's argument that Egel-Matani et al do not teach the specific aspartic protease SPCC1795.09 as described in the specification, such an argument is not germane because the instant claims do not recite the use of this specific protease; rather the instant claims encompass the use of any aspartic protease.

Claims 14, 17, 19, 20, 23 and 25 are rejected under 35 U.S.C. 102(b) as being anticipated by Simeon et al (Yeast 11:271-282, 1995; IDS Ref. AW). **This rejection is maintained for reasons of record.**

Response to Arguments

Applicant concedes that the Simeon et al publication appears to describe a CPY serine protease. However, Applicant argues that Simeon does not describe the specific serine protease isp6 (SPAC1F8.07) which has a sequence which is different and distinct in structure from that of carboxypeptidase Y.

Applicant's arguments have been carefully considered but have respectfully been found unpersuasive. Applicant's arguments are directed to claims which are limited to the

specific serine protease isp6; however the instant claims encompass any serine protease (see claims 17 and 23) as well as any carboxypeptidase (see claims 14, 19-20 and 25).

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 14, 18, 20 and 24 are rejected under 35 U.S.C. 103(a) as being unpatentable over Berka et al (WO 00/42203; of record) in view of Giga-Hama et al (*Biotechnol. Appl. Biochem.* **30**:235-244, 1999; of record). **This rejection is maintained for reasons of record.**

Response to Arguments

Applicant argues that this rejection is no longer applicable in light of the amended claims and particularly because these two publications do not describe or suggest the specific genes/enzymes defined in claims 14 and 20.

Applicant's arguments have been carefully considered and have respectfully been found unpersuasive because the instant claims have not been narrowed in scope by amendment with regard to the genus of aminopeptidases encompassed. Therefore claims 14, 18, 20 and 24 remain unpatentable over the Berka et al and Giga-Hama et al references.

Claims 14-15 and 20-21 are rejected under 35 U.S.C. 103(a) as being unpatentable over Rajgarhia et al (US Patent Application Publication 2003/0166179 A1) in view of Giga-Hama et al (*Biotechnol. Appl. Biochem.* **30**:235-244, 1999; of record).

This is a new rejection not necessitated by Applicant's amendment.

Rajgarhia et al teach a method of constructing a yeast host cell which produces a heterologous protein comprising deleting or inactivating at least one host gene including pyruvate decarboxylase (including PDC1 of any number of yeast cells including *Saccharomyces cerevisiae* and *K. thermotolerans*, *K. marxianus*, *C. sonorensis*, etc.) and transforming the host cell with a polynucleotide which encodes the heterologous protein (see entire document, especially page 1, paragraphs [0005]-[0006], page 2, paragraphs [0015] and [0019]-[0020]; page 6, paragraph [0074]; page 8, paragraph [0083]; page 17, Example 6; page 22, Example 18; page 32, paragraphs [0305]-[0311]). In addition, Rajgharia et al teach that yeast cells having the ability to grow in the absence of ethanol and acetate while lacking the ability to produce ethanol can redirect the utilization of pyruvate to produce organic products other than ethanol. Finally, Rajgarhia et al teach that it is desirable to delete the PDC genes in strains to be used for lactic acid production (see page 32, paragraph [0305]) and Rajgarhia et al also teach that cells for lactate production can be transformed with a heterologous lactate dehydrogenase gene (see, e.g., the Abstract). While Rajgarhia et al do not explicitly teach such a

method wherein the inactivation of the pyruvate decarboxylase results in increased heterologous *protein* production, such would inherently be the case based upon Applicant's admission in the specification that "deletion or inactivation of part or all of the genome of the host unnecessary or detrimental to production of the heterologous protein by its transformation improves the production efficiency of the heterologous protein" (see instant specification at page 3, lines 24-27 and page 4, line 1).

Rajgarhia et al do not teach such a method for an *S. pombe* host cell.

Giga-Hama et al teach the use of *S. pombe* as a host for expression and production of foreign genes. Giga-Hama et al teach that there are several advantages to the use of *S. pombe* (see entire document, especially page 237, 2nd column, first paragraph). First, Giga-Hama teach that the *S. pombe* yeast has many characteristics more in common with higher mammalian cells than with other yeasts which makes this yeast host a good model for higher eukaryotic protein production and yields foreign gene products that are "closer to their natural form" (page 237, 2nd column, first-third paragraphs). Second, Giga-Hama et al teach that there are a number of vectors and promoters which result in efficient expression of a heterologous protein (see pages 239-240 and Table 1). Finally, Giga-Hama teach that *S. pombe* is a

good host for the production of a number of different proteins (see, e.g., page 241, Table 2).

It would have been obvious to combine the teachings of Rajgarhia et al with those of Giga-Hama et al because Rajgarhia et al teach the expression of exogenous proteins in yeast cells for production and collection of the heterologous protein and Giga-Hama teaches that *S. pombe* is a good yeast cell for foreign protein production.

One of ordinary skill in the art would have been motivated to combine the teachings of Rajgarhia et al and Giga-Hama et al because Giga-Hama et al teach that there are advantages of using the *S. pombe* cell, especially in cases where the heterologous gene to be produced is a mammalian protein because the mammalian protein would be "closer to [its] nature form." Moreover, Rajgarhia et al teach that use of a host with reduced pyruvate decarboxylase activity is advantageous when, for example, the host cell is to be used in lactic acid production or in situations wherein the utilization of pyruvate can be redirected toward the production of the organic compound to be produced.

Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation

of success to result when combining the teachings of Rajgarhia et al with those of Giga-Hama et al.

Conclusion

No claim is allowed.

Certain papers related to this application may be submitted to the Art Unit 1636 by facsimile transmission. The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 C.F.R. § 1.6(d)). The official fax telephone number for the Group is (571) 273-8300. Note: If Applicant *does* submit a paper by fax, the original signed copy should be retained by Applicant or Applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify

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For all other customer support, please call the USPTO Call Center (UCC) at (800) 786-9199.

Any inquiry concerning rejections or objections in this communication or earlier communications from the examiner should be directed to Walter Schlapkohl whose telephone number is (571) 272-4439. The examiner can normally be reached on Monday through Friday from 8:30 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Joseph Woitach can be reached at (571) 272-0739.

Walter A. Schlapkohl, Ph.D.
Patent Examiner
Art Unit 1636

July 7, 2007

DAVID GUZO
PRIMARY EXAMINER

Display Summary Show 20 Sort by Relevance

All: 17 Bacteria: 0 RefSeq: 0 Related Structures: 16

Items 1 - 17 of 17

1: CAA91125 Reports BLink, Conserved I
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Items 1 - 17 of 17

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VERSION     CAA91125.1  GI:3859775
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  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
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  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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Cerutti L]]
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AUTHORS Badcock,K. and Churcher,C.M.
JOURNAL Unpublished
REFERENCE 3 (residues 1 to 389)
AUTHORS Barrell,B.G., Rajandream,M.A., Walsh,S.V. and Wood,V.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1995) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: pombe@sanger.ac.uk
COMMENT On Nov 11, 1998 this sequence version replaced gi:1015927.
Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.
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/note="Creatinase/Prolidase N-terminal domain. This family includes the N-terminal non-catalytic domains from creatinase and prolidase. The exact function of this domain is uncertain; pfam01321"
/db_xref="CDD:65142"
Region 310..>389
/region_name="APP"
/note="X-Prolyl Aminopeptidase 2. E.C. 3.4.11.9. Also known as X-Pro aminopeptidase, proline aminopeptidase, aminopeptidase P, and aminoacylproline aminopeptidase; cd01085"

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                     /db_xref="CDD:29970"
     CDS             1..389
                     /gene="SPAC22G7.01c"
                     /coded_by="complement(join(Z54328.1:<1..1022,
                     Z54328.1:1137..1192,Z54328.1:1278..1367))"
                     /note="aminopeptidase (predicted); peptidase family M24;
                     similar to S. cerevisiae YLL029W"
                     /db_xref="GOA:Q09795"
                     /db_xref="UniProtKB/Swiss-Prot:Q09795"
ORIGIN
        1 mvvhtgnrln klrelmkerg ytlyvvpsed ahsseytcda darrafisgf dgsagcavig
       61 etsaalftdg ryfnqasqql denwtlmkqg ftgvptweey ctqmtkcnek vgidsslitf
      121 paakalresl flksgavlvg dhdnlvdivw gasrpkeple klivqeikya glgvdeklhn
      181 lreamkeqki eafvvsmlde vawlynlrga dvpynpvffa yslvtldeaf lyvderkvtp
      241 evskhldgfv kilpydrvfs daknsnltri gissktswci atsfgetkvm pilspisqak
      301 gikndaelkg mkechirdgc alveyfawld eylnsgnkin efdaatkleq frrknnlfmg
      361 lsfetisstg pngavihysp patgsaiid
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1: CAB62423. Reports SPAC22G7.01c [Sch...[gi:32139912].

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAB62423                242 aa            linear   PLN 16-APR-2005
DEFINITION  SPAC22G7.01c [Schizosaccharomyces pombe].
ACCESSION   CAB62423
VERSION     CAB62423.2  GI:32139912
DBSOURCE    embl accession AL133359.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 242)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
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            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
            Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,
            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
            Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,
            Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
            Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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            Cerutti L]]
REFERENCE   2  (residues 1 to 242)
  AUTHORS   McDougall,R.C., Rajandream,M.A., Barrell,B.G., Brown,S. and
            Harris,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-1999) European Schizosaccharomyces genome
            sequencing project, Sanger Institute, The Wellcome Trust Genome
            Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk
COMMENT     On Jun 21, 2003 this sequence version replaced gi:6562186.
            Notes:
            Details of S. pombe sequencing at the Sanger Institute are
            available on the World Wide Web.
            (URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL,
            http://www.sanger.ac.uk/Projects/S_pombe/)
            CDS are numbered using the following system eg SPAC5H10.01c. SP (S.
            pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c
            (complementary strand). However, clones may have been reorientated
            since the original submission, therefore the complementary strand
            notation may be invalid for strand inference.
            IMPORTANT: This sequence MAY NOT be the entire insert of the
            sequenced clone.  It may be shorter because we only sequence
            overlapping sections once.
FEATURES             Location/Qualifiers
     source          1..242
                     /organism="Schizosaccharomyces pombe"
                     /strain="972h-"
                     /db_xref="taxon:4896"
                     /chromosome="I"
                     /map="IL"
     Protein         1..242
                     /name="SPAC22G7.01c"
     Region          <1..178
                     /region_name="APP"
                     /note="X-Prolyl Aminopeptidase 2. E.C. 3.4.11.9. Also
                     known as X-Pro aminopeptidase, proline aminopeptidase,
                     aminopeptidase P, and aminoacylproline aminopeptidase;
                     cd01085"
                     /db_xref="CDD:29970"
     CDS             1..242
                     /gene="SPAC22G7.01c"
                     /coded_by="complement(AL133359.1:4676..>5404)"
                     /db_xref="GOA:Q09795"
                     /db_xref="UniProtKB/Swiss-Prot:Q09795"
ORIGIN
        1 lfmglsfeti sstgpngavi hysppatgsa iidptkiylc dsgaqykdgt tdvtrtwhfg
       61 epseferqta tlalkghial anivfpkgtt gymidvlarq ylwkygldyl hgtghgvgsf
      121 lnvhelpvgi gsrevfnsap lqagmvtsne pgfyedghfg yrvencvyit evntenrfag
      181 rtylglkdlt laphcqklid psllspeevk ylneyhsevy ttlspmlsvs akkwlskhts
      241 pi
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☐ 1: CAA90806. Reports SPAC13A11.05 [Sch...[gi:984226]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA90806                 513 aa            linear   PLN 18-APR-2005
DEFINITION  SPAC13A11.05 [Schizosaccharomyces pombe].
ACCESSION   CAA90806
VERSION     CAA90806.1  GI:984226
DBSOURCE    embl accession Z54096.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 513)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
            Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
            Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,
            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
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            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
```

Cerutti L]]
REFERENCE 2 (residues 1 to 513)
AUTHORS Hunt,S., Devlin,K., Churcher,C.M., Barrell,B.G., Rajandream,M.A. and Walsh,S.V.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1995) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Institute, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: pombe@sanger.ac.uk
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.
FEATURES Location/Qualifiers
source 1..513
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="I"
/map="IL"
/clone="cosmid c13A11"
Protein 1..513
/name="SPAC13A11.05"
Region 28..513
/region_name="PepB"
/note="Leucyl aminopeptidase [Amino acid transport and metabolism]; COG0260"
/db_xref="CDD:30609"
Region 31..508
/region_name="Peptidase_M17"
/note="Cytosol aminopeptidase family, N-terminal and catalytic domains. Family M17 contains zinc- and manganese-dependent exopeptidases (EC 3.4.11.1), including leucine aminopeptidase; cd00433"
/db_xref="CDD:48344"
CDS 1..513
/gene="SPAC13A11.05"
/coded_by="Z54096.1:8608..10149"
/note="cytosol aminopeptidase; peptidase family M17; no apparent S. cerevisiae ortholog"
/db_xref="GOA:Q09735"
/db_xref="InterPro:IPR000819"
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/db_xref="InterPro:IPR011356"
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ORIGIN
1 mkglglstrt fnwsslssil lpriplattk adslilavrh dkqvfsedyr qvvdqyfets
61 pkkndirlfw ntqgfvrlai vqleenvsek svrsaaaeaa kilksngaks iavdgmgfpk
121 daalgaalat ydfslrrdhl svyqdekvve kenlftspap erltfqllsn tsekktatae
181 enafkvglie aaaqnlarsl mecpanymts lqfchfaqel fqnsskvkvf vhdekwideq
241 kmnglltvna gsdipprfle vqyigkeksk ddgwlglvgk gvtfdsggis ikpsqnmkem
301 radmggaavm lssiyaleql sipvnavfvt pltenlpsgs aakpgdvifm rnglsveidn

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      361 tdaegrlila davhyvssqy ktkavieast ltgamlvalg nvftgafvqg eelwknleta
      421 shdagdlfwr mpfheaylkq ltsssnadlc nvsragggcc taaafikcfl aqkdlsfahl
      481 diagvmdkql nswdcdgmsg rpvrtiieva rky
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Jun 19 2007 13:56:00

☐ 1: CAA19013. Reports SPBC3E7.10 [Schiz...[gi:3130036]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA19013                379 aa            linear   PLN 16-APR-2005
DEFINITION  SPBC3E7.10 [Schizosaccharomyces pombe].
ACCESSION   CAA19013
VERSION     CAA19013.1  GI:3130036
DBSOURCE    embl accession AL023534.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 379)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
            Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
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            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
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            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
            Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,
            Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
            Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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Cerutti L]]
REFERENCE 2 (residues 1 to 379)
AUTHORS Lyne,M., Wood,V., Rajandream,M.A., Barrell,B.G., Brown,D. and Churcher,C.M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-1998) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers

source 1..379
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="II"
/map="IIR"
/clone="cosmid c3E7"

Protein 1..379
/EC_number="3.4.11.18"
/name="SPBC3E7.10"

Region 126..367
/region_name="MetAP1"
/note="Methionine Aminopeptidase 1. E.C. 3.4.11.18. Also known as methionyl aminopeptidase and Peptidase M. Catalyzes release of N-terminal amino acids, preferentially methionine, from peptides and arylamides; cd01086"
/db_xref="CDD:29971"

CDS 1..379
/gene="SPBC3E7.10"
/coded_by="join(AL023534.1:23540..23656, AL023534.1:23709..23729,AL023534.1:23779..23824, AL023534.1:23885..24840)"
/note="methionine aminopeptidase (predicted); similar to S. cerevisiae MAP1"
/db_xref="GOA:O59730"
/db_xref="InterPro:IPR000994"
/db_xref="InterPro:IPR001714"
/db_xref="InterPro:IPR002467"
/db_xref="UniProtKB/Swiss-Prot:O59730"

ORIGIN

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        1 mateiakhic cgidcnnead rlqcpkclnd gvksyfcgqe cfrnswnihk hlhrppnvek
       61 redgtynpfp kfhfagslkp vyplspirkv pphikrpdya ktgvsrseqi egrsfklkrl
      121 tpkeqegmrk vcrlgrevld aaaaavrpgt ttdeldsivh nacierdcfp stlnyyafpk
      181 svctsvneii chgipdqrpl edgdivnidv slyhngfhgd lnetyyvgdk akanpdlvcl
      241 ventrialdk aiaavkpgvl fqefgniiek htnsitekqi svvrtycghg inqlfhcsps
      301 iphyshnkap giarpgmtft iepmltlgpa rditwpddwt sstasgrcsa qfehtllvte
      361 tgcevltarl pnspggplk
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Jun 19 2007 13:56:00

1: CAA94695. Reports SPAC12B10.05 [Sch...[gi:4008582]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA94695                 486 aa            linear   PLN 18-APR-2005
DEFINITION  SPAC12B10.05 [Schizosaccharomyces pombe].
ACCESSION   CAA94695
VERSION     CAA94695.1  GI:4008582
DBSOURCE    embl accession Z70721.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 486)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
            Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
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            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
            Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,
            Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
            Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
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            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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            Cerutti L]]
REFERENCE   2  (residues 1 to 486)
  AUTHORS   Badcock,K. and Churcher,C.M.
  JOURNAL   Unpublished
REFERENCE   3  (residues 1 to 486)
  AUTHORS   Barrell,B.G., Rajandream,M.A. and Walsh,S.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-1996) Schizosaccharomyces pombe chromosome I
            sequencing project, Sanger Institute, Hinxton Hall, Hinxton,
            Cambridge CB10 1RQ.E-mail: pombe@sanger.ac.uk
COMMENT     Notes:
            Details of S. pombe sequencing at the Sanger Institute are
            available on the World Wide Web.
            (URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL,
            http://www.sanger.ac.uk/Projects/S_pombe/)
            CDS are numbered using the following system eg SPAC5H10.01c. SP (S.
            pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c
            (complementary strand). However, clones may have been reorientated
            since the original submission, therefore the complementary strand
            notation may be invalid for strand inference.
            IMPORTANT: This sequence MAY NOT be the entire insert of the
            sequenced clone.  It may be shorter because we only sequence
            overlapping sections once.
FEATURES             Location/Qualifiers
     source          1..486
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                     /db_xref="CDD:30356"
     Region          62..198
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                     /note="Aminopeptidase P, N-terminal domain. This domain is
                     structurally very similar to the creatinase N-terminal
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                     similarity exists between the two families; pfam05195"
                     /db_xref="CDD:68756"
     Region          240..472
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                     /note="Prolidase. E.C. 3.4.13.9. Also known as Xaa-Pro
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                     hydrolysis of Xaa-Pro dipeptides; also acts on
                     aminoacyl-hydroxyproline analogs; cd01087"
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                     Z70721.1:10621..10653,Z70721.1:10697..10824,
                     Z70721.1:10864..11247,Z70721.1:11309..11386,
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                     Z70721.1:11430..11651,Z70721.1:11701..11808,
                     Z70721.1:11853..12023)"
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                     /db_xref="InterPro:IPR000994"
                     /db_xref="InterPro:IPR001131"
                     /db_xref="InterPro:IPR007865"
                     /db_xref="UniProtKB/Swiss-Prot:Q10439"
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        1 msgyirtlfi rnrfsnyrlr sqiikykysn vsylnksalr cgqatdsthp hilqpgeltp
       61 risaqeyktr rdrvaslled ndfmivtsap vrhmcgaafy eyhqdpnfyy ltgclepnav
      121 llmfkngasg sydcslylps knpyiekweg lrtgstlgkk lfqienvyds slassvinal
      181 gkksnrifyn yqtgylskmp aasapefiqd tltklfrtst qrsvdellhp lrsikstael
      241 ecmkeaanis snvyreimrk rfekeaemsa efnyrfcigg cdrsayvpvv aggkngltih
      301 ytinndifrp demvlvdagg efggyvtdis rtwpingkfs tvqrdlyqav lnvqkkciky
      361 cctsngwsla dihfesvklm heelkqvgih gtkreitdil yphsigheig leihdcstnn
      421 gyqplrknqv itiepglyvp eedgwpqwaq giairiedsv ivgddkpfvl tsaapkeiee
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☐ 1: CAB11706. Reports SPAC4F10.02 [Schi...[gi:2388974]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAB11706                467 aa            linear   PLN 18-APR-2005
DEFINITION  SPAC4F10.02 [Schizosaccharomyces pombe].
ACCESSION   CAB11706
VERSION     CAB11706.1  GI:2388974
DBSOURCE    embl accession Z98980.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 467)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
            Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
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            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
```

Cerutti L]]
REFERENCE 2 (residues 1 to 467)
AUTHORS Connor,R., Churcher,C.M., Barrell,B.G., Rajandream,M.A. and Wood,V.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1997) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Institute, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: pombe@sanger.ac.uk
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.
FEATURES Location/Qualifiers
source 1..467
/organism="Schizosaccharomyces pombe"
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181 pliglenela keetsdngdk yhhpvllsll aneiskslet tidpskivdf elilgdaeka
241 rlggiheefv fsprldnlgm tfcasqaltk slennsldne scvrvvpsfd heeigsvsaq
301 gaestflpav lqricelgke sslfsismvk sflvsadmah amhpnyssry ensntpflnk
361 gtvikvnanq ryttnsagiv llkkvaqlad vpiqsfvvrn dspcgstigp klaamtgmrt
421 ldlgnpmlsm hscremcgsk dfeyavvlfs sffqnfanle ekiiide
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1: CAB58971. Reports SPBC1921.05 [Schi...[gi:6090559]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAB58971                882 aa            linear   PLN 16-APR-2005
DEFINITION  SPBC1921.05 [Schizosaccharomyces pombe].
ACCESSION   CAB58971
VERSION     CAB58971.1  GI:6090559
DBSOURCE    embl accession AL122033.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast).
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 882)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
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            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
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            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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            Cerutti L]]
REFERENCE   2  (residues 1 to 882)
  AUTHORS   Seeger,K., Harris,D., McDougall,R.C., Rajandream,M.A. and
            Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) European Schizosaccharomyces genome
            sequencing project, Sanger Institute, The Wellcome Trust Genome
            Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and
COMMENT     Notes:
            Details of S. pombe sequencing at the Sanger Institute are
            available on the World Wide Web.
            (URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL,
            http://www.sanger.ac.uk/Projects/S_pombe/)
            CDS are numbered using the following system eg SPAC5H10.01c. SP (S.
            pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c
            (complementary strand). However, clones may have been reorientated
            since the original submission, therefore the complementary strand
            notation may be invalid for strand inference.
            IMPORTANT: This sequence MAY NOT be the entire insert of the
            sequenced clone.  It may be shorter because we only sequence
            overlapping sections once.
FEATURES             Location/Qualifiers
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                     /db_xref="CDD:30656"
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      481 lieqhrflst gdvkpeedtv iywaplklkt mkdgkavvde kavlsdrskk ikvdkeales
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      661 kanddhiirq fkstvynyag lfgddkvvkd alskfdayas gnksaindnl rsavfniair
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Jun 19 2007 13:56:00

☐ 1: CAA21804. Reports SPBP8B7.19 [Schiz...[gi:3810843]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA21804                1019 aa            linear   PLN 16-APR-2005
DEFINITION  SPBP8B7.19 [Schizosaccharomyces pombe].
ACCESSION   CAA21804
VERSION     CAA21804.1  GI:3810843
DBSOURCE    embl accession AL032684.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 1019)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
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            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
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            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
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            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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Cerutti L]]
REFERENCE 2 (residues 1 to 1019)
AUTHORS Beck,A., Reinhardt,R., Lyne,M., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1998) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and Max Planck Institut fuer Molekulare Genetik, Ihnestr. 73, D-14195 Berlin, Germany
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES	Location/Qualifiers
source	1..1019
	/organism="Schizosaccharomyces pombe"
	/strain="972h-"
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	/chromosome="II"
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Protein	1..1019
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Region	1..935
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Region	181..427
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Region	838..>920
	/region_name="Rtt106"
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	/gene="SPBP8B7.19"

/coded_by="AL032684.1:38931..41990"
/note="peptidase family M24 (inferred from context);
involved in chromatin mediated transcriptional regulation
(predicted); involved in cell cycle control (predicted);
global transcription factor C; similar to S. cerevisiae
SPT16"
/db_xref="GOA:O94267"
/db_xref="InterPro:IPR000994"
/db_xref="UniProtKB/Swiss-Prot:O94267"

ORIGIN

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      361 giefressll vnaknprvlq agmtlnlsig fgnlinphpk nsqskeyall lidtiqitrs
      421 dpivftdspk aqgdisyffg eddssledgv kprkpptrgt atisshkgkt rsetrdldds
      481 aekrrvehqk qlasrkqaeg lqrfaqgsvp ssgiekptvk rfesykrdsq lpqaigelri
      541 lvdyraqsii lpifgrpvpf histlknask ndegnfvylr lnfvspgqig gkkdelpfed
      601 pnaqfirsft frssnnsrms qvfkdiqdmk kaatkreter kefadvieqd klieiknkrp
      661 ahindvyvrp aidgkrlpgf ieihqngiry qsplrsdshi dllfsnmkhl ffqpcegeli
      721 vlihvhlkap imvgkrktqd vqfyrevsdi qfdetgnkkr kymygdedel eqeqeerrrr
      781 aqldrefksf aekiaeaseg rieldipfre lafngvpfrs nvllqpttdc lvqltdtpft
      841 vitlneieia hlervqfglk nfdlvfifqd frrppihint ipmeqldnvk ewldscdicf
      901 yegplnlnwt timktvnedp iaffeeggwg flgapsddeg ddsveevsey easdadpsde
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☐ 1: CAA18421. Reports SPBC14C8.03 [Schi...[gi:3006161]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA18421                 426 aa            linear   PLN 16-APR-2005
DEFINITION  SPBC14C8.03 [Schizosaccharomyces pombe].
ACCESSION   CAA18421
VERSION     CAA18421.1  GI:3006161
DBSOURCE    embl accession AL022305.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 426)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
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            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
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            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
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            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
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            Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
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            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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Cerutti L]]
REFERENCE 2 (residues 1 to 426)
AUTHORS Lyne,M., Rajandream,M.A., Barrell,B.G. and Volckaert,G.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-1998) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and Katholieke Universiteit Leuven, Faculty of Agricultural and Applied Biological Sciences, Laboratory of Gene Technology, Kardinaal Mercierlaan 92 Blok F, B-3001 Leuven, Belgium
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers
source 1..426
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="II"
/map="IIR"
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Protein 1..426
/EC_number="3.4.11.18"
/name="SPBC14C8.03"
Region 114..422
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/note="Methionine Aminopeptidase 2. E.C. 3.4.11.18. Also known as methionyl aminopeptidase and peptidase M. Catalyzes release of N-terminal amino acids, preferentially methionine, from peptides and arylamides; cd01088"
/db_xref="CDD:29973"
CDS 1..426
/gene="SPBC14C8.03"
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/db_xref="GOA:O60085"
/db_xref="HSSP:P50579"
/db_xref="InterPro:IPR000994"
/db_xref="InterPro:IPR001714"
/db_xref="InterPro:IPR002468"
/db_xref="UniProtKB/TrEMBL:O60085"

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1 mtsattteat akdlqeklsl kendvveddg kveendaaee gasngekkkk kkkksskkkk
61 tpqeqtnppt vglskifvnk kypvgevcdy aednlwrttd eekraldrqn fdqyndlrra
121 aevhrqarqy aqsvikpgms mmdvvntien ttralveedg lksgigfptg vslnhcaahy
181 tpnagdttil kekdvmkvdi gvhvngrivd saftmsfdpq ydnllaavka atnkgieeag
241 idarlneige aiqevmesye veingkthqv ksirnlcghn ldpyiihggk svpivkggee
301 ikmeegeifa ietfgstgrg vvhedmecsh yakipdaghi plrlprakal lntitqnfgt

```
      361 lpfcrryldr igeskyllal nnlvsagivq dypplcdirg sytaqfehti ilhptqkevv
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//
```


Jun 19 2007 13:56:00

☐ 1: CAB45933. Reports SPBC18A7.01 [Schi...[gi:5263087]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAB45933                451 aa            linear   PLN 20-JUN-2003
DEFINITION  SPBC18A7.01 [Schizosaccharomyces pombe].
ACCESSION   CAB45933
VERSION     CAB45933.1  GI:5263087
DBSOURCE    embl accession AL080287.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 451)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
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            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
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            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
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            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
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            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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Cerutti L]]
REFERENCE 2 (residues 1 to 451)
AUTHORS Wood,V., Rajandream,M.A., Barrell,B.G. and Moreno,S.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1999) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and Instituto de Microbiologia Bioquimica, CSIC Universidad de Salamanca, Edificio Departamental, Campus Miguel de Unamuno, 37007 Salamanca, Spain
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers

source 1..451
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="II"
/map="IIR"
/clone="cosmid c18A7"

Protein 1..451
/name="SPBC18A7.01"

Region 227..432
/region_name="APP-like"
/note="Similar to Prolidase and Aminopeptidase P. The members of this subfamily presumably catalyse hydrolysis of Xaa-Pro dipeptides and/or release of any N-terminal amino acid, including proline, that is linked with proline; cd01092"
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CDS 1..451
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/coded_by="AL080287.1:892..2247"
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/db_xref="GOA:Q9UUD8"
/db_xref="InterPro:IPR000994"
/db_xref="InterPro:IPR001131"
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     1 mvsfessfer gtdflnrnfk kclfacisif ifallalsfl sllqpdtvqr lyqcavpsmi
    61 yvppmineai siqheefnnr rrrlsaalre dkldalimep tvsmdyfani ttgswglser
   121 pflgiifsdd epypgdvasr iyflvpkfel prakelvgkn idakyitwde denpyqvlyd
   181 rlgplklmid gtvrnfiaqg lqyagfttfg vsprvaslre ikspaevdim srvniatvaa
   241 irsvqpcikp gitekelaev inmlfvyggl pvqespivlf geraamphgg psnrrlkkse
   301 fvlmdvgttl fgyhsdctrt vlphgqkmte rmeklwnlvy daqtagiqml shlsntscae
   361 vdlaarkvik dagygeyfih rlghglglee heqtylnpan kgtpvqkgnv ftvepgiyip
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      421 deigirieda vlasdvpill tnfrakspye p
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Jun 19 2007 13:56:00

☐ 1: CAB08750. Reports SPAC3A12.05c [Sch...[gi:14422268]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAB08750                1174 aa            linear   PLN 18-APR-2005
DEFINITION  SPAC3A12.05c [Schizosaccharomyces pombe].
ACCESSION   CAB08750
VERSION     CAB08750.2  GI:14422268
DBSOURCE    embl accession Z95395.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 1174)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
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            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
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            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
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            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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Cerutti L]]
REFERENCE 2 (residues 1 to 1174)
AUTHORS Badcock,K. and Churcher,C.M.
JOURNAL Unpublished
REFERENCE 3 (residues 1 to 1174)
AUTHORS Wood,V., Barrell,B.G. and Rajandream,M.A.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-1997) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Institute, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: pombe@sanger.ac.uk
COMMENT On Jun 13, 2001 this sequence version replaced gi:2104421.
Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers

source 1..1174
/organism="Schizosaccharomyces pombe"
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/db_xref="taxon:4896"
/chromosome="I"
/map="IL"
/clone="cosmid c3A12"

Protein 1..1174
/name="SPAC3A12.05c"

Region 2..>763
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/note="Aminopeptidase N [Amino acid transport and metabolism]; COG0308"
/db_xref="CDD:30656"

CDS 1..1174
/gene="SPAC3A12.05c"
/coded_by="complement(join(Z95395.1:6860..7795, Z95395.1:7836..10264,Z95395.1:10356..10483, Z95395.1:10529..10560))"
/note="transcription initiation factor activity; transcription factor TFIID complex (predicted); histone fold; involved in transcription from Pol II promoter; similar to S. cerevisiae YCR042C"
/db_xref="GOA:P87121"
/db_xref="InterPro:IPR001930"
/db_xref="UniProtKB/TrEMBL:P87121"

ORIGIN

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      121 ivsidfsvhq pifgitfvgi dpvdhryphv ftnnsiipys tcswlpcvdg iwerstwefe
      181 itlpktlssl mhrektqpsd lnngangvdg hddnyennrf dhqfnlsnep dlledhdiev
      241 iccgdlldqv thpkdmrkkt vyfsvttpva pnyiafaagp fkhinltdfr epedddamgs
      301 saiditgyyl pkyaeevent cvflykamdf fvreygsypf nsfklcfvde tnfpiistps
      361 lvissnsily pkdsldqiyd stktltwala sqwigvylip kawsdlwliy glsyyicglf
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 601 fsgpmtirih eadgtpyehv velkdsftkl diqyntkykr isrnrstknv krdgdhngdd
 661 sdyvirslgd vlqsdedier whlydytkee edtmateafe wirvdadfew icdlrvrqpe
 721 hmyvsqlqqd rdvvaqleti rhftsesftv sqqvstvllr tlldnryyyg irqeaarala
 781 rcaipeldwv gyyhlrmayl ekfcfkdsti pksndfsnit eyyvkcamle sfpnirdrkg
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 901 vnqvineidr ymridacmps fkniitcksl kaklrlaqtf hlefgpkell pytqegnyvl
 961 vrciafnlml qagalkytpl ikyifyiltn dlspvvrrsl lysvqdglga larggtksdv
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1081 tkrnllmicr vlykakssll vtlkipslip rlraihlgkg kivikkaplk qitsktkeks
1141 tsptppsiti npikpkgptl kikltnlrst ppsh
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☐ 1: CAB11208. Reports SPAC14C4.15c [Sch...[gi:2330688]

LOCUS CAB11208 743 aa linear PLN 18-APR-2005
DEFINITION SPAC14C4.15c [Schizosaccharomyces pombe].
ACCESSION CAB11208
VERSION CAB11208.1 GI:2330688
DBSOURCE embl accession Z98596.1
KEYWORDS .
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
Schizosaccharomycetes; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE 1 (residues 1 to 743)
AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
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Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
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Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
Ussery,D., Barrell,B.G. and Nurse,P.
TITLE The genome sequence of Schizosaccharomyces pombe
JOURNAL Nature 415 (6874), 871-880 (2002)
PUBMED 11859360
REMARK Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]
REFERENCE 2 (residues 1 to 743)
AUTHORS Devlin,K., Churcher,C.M., Barrell,B.G., Rajandream,M.A. and Wood,V.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-1997) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: pombe@sanger.ac.uk
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers

source 1..743
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="I"
/map="IR"
/clone="cosmid c14C4"

Protein 1..743
/name="SPAC14C4.15c"

Region 5..743
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/db_xref="CDD:31695"

Region 72..433
/region_name="DPPIV_N"
/note="Dipeptidyl peptidase IV (DPP IV) N-terminal region. This family is an alignment of the region to the N-terminal side of the active site. The Prosite motif does not correspond to this Pfam entry; pfam00930"
/db_xref="CDD:64779"

Region 570..735
/region_name="Peptidase_S9"
/note="Prolyl oligopeptidase family; pfam00326"
/db_xref="CDD:64203"

CDS 1..743
/gene="SPAC14C4.15c"
/coded_by="complement(join(Z98596.1:33862..34966, Z98596.1:35011..>36138))"
/note="dipeptidyl aminopeptidase (predicted); similar to S. cerevisiae YHR028C and YOR219C"
/codon_start=2
/db_xref="GOA:Q9P7E9"
/db_xref="UniProtKB/Swiss-Prot:Q9P7E9"

ORIGIN
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61 ltcknlhrkr yssdmeyiaf scskdrrwrh syyedvylve ratgriehla sdqskkivva
121 ewspighklv yglgsnlfiw esfseppvci tdqsdldglf ngnsdwvyee eilqsskavw
181 wspdgnclsy lsiddskvpv hvlpfeqlds kvedqnrvnn ffhystpkdp ipfvklfvnc

```
241 ftdsgesiev dssfplstqh ryitdvawag neklmfvevl rgnyervtsl fdlssrktti
301 entevsehpl altsslhlky lsfeslgnlk eryvrqyfls nkkriaiyel dnpvpiyltp
361 vnisflsdly linntlyfta issgspfsrv yrlctkslil seiniqigsg lfgikvsndq
421 nyllvnylgp eipkqfiysi hedkvstsnd hsknnlpsds sstslgkvkl elcnsletne
481 eliitkekfa fpsvffkvik vknitayiqe irppnfnprk ryptvfhlyg apqsalvtgk
541 yemdinelma svynflvikv divdisdvsg qhlfsdshel iikswiellr syvdtpyidr
601 hrvgiwgwsf ggyltlkile nadfiktgav vapvtdwryy dayysenllg ayskqttaiy
661 dktavhysen frklcgllvl hgtsddnvhi entmqltkam vekgvynyyp fivpnanhef
721 sdptdytflr eklsghfhha lyc
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Jun 19 2007 13:56:00

☐ 1: CAA20739. Reports SPBC18A7.01 [Schi...[gi:6782390]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA20739                 243 aa            linear   PLN 16-APR-2005
DEFINITION  SPBC18A7.01 [Schizosaccharomyces pombe].
ACCESSION   CAA20739
VERSION     CAA20739.2  GI:6782390
DBSOURCE    embl accession AL031534.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 243)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
            Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
            Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,
            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
            Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,
            Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
            Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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Cerutti L]]
REFERENCE 2 (residues 1 to 243)
AUTHORS Gwilliam,R., Rajandream,M.A., Barrell,B.G., Skelton,J. and Churcher,C.M.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1998) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk
COMMENT On Jan 27, 2000 this sequence version replaced gi:3560152.
Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers
source 1..243
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="II"
/map="IIR"
/clone="cosmid c4F6"
Protein 1..243
/name="SPBC18A7.01"
Region 90..>242
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/note="Xaa-Pro aminopeptidase [Amino acid transport and metabolism]; COG0006"
/db_xref="CDD:30356"
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/coded_by="AL031534.1:44051..>44778"
/db_xref="GOA:Q9UUD8"
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ORIGIN
1 mvsfessfer gtdflnrnfk kclfacisif ifallalsfl sllqpdtvqr lyqcavpsmi
61 yvppmineai siqheefnnr rrrlsaalre dkldalimep tvsmdyfani ttgswglser
121 pflgiifsdd epypgdvasr iyflvpkfel prakelvgkn idakyitwde denpyqvlyd
181 rlgplklmid gtvrnfiaqg lqyagfttfg vsprvaslre ikspaevdim srvniatvaa
241 irs
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☐ 1: CAA22858. Reports SPCC1322.05c [Sch...[gi:4176545]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA22858                612 aa            linear   PLN 16-APR-2005
DEFINITION  SPCC1322.05c [Schizosaccharomyces pombe].
ACCESSION   CAA22858
VERSION     CAA22858.1  GI:4176545
DBSOURCE    embl accession AL035259.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 612)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
            Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
            Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,
            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
            Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,
            Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
            Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
```

Cerutti L]]
REFERENCE 2 (residues 1 to 612)
AUTHORS Lucas,M., Gaillardin,C., Lyne,M., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1999) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and INRA - CBAI, Laboratoire de Genetique Moleculaire et Cellulaire, Route de Thiverval, F-78850 Thiverval Grignon, France
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers

source 1..612
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="III"
/map="IIIR"
/clone="cosmid c1322"

Protein 1..612
/EC_number="3.3.2.6"
/name="SPCC1322.05c"

Region 15..>612
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/note="Aminopeptidase N [Amino acid transport and metabolism]; COG0308"
/db_xref="CDD:30656"

Region 464..608
/region_name="Leuk-A4-hydro_C"
/note="Leukotriene A4 hydrolase, C-terminal; pfam09127"
/db_xref="CDD:72544"

CDS 1..612
/gene="SPCC1322.05c"
/coded_by="complement(AL035259.1:9003..10841)"
/note="leukotriene A-4 hydrolase (predicted); similar to S. cerevisiae YNL045W"
/db_xref="GOA:O94544"
/db_xref="InterPro:IPR001930"
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ORIGIN

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      121 kpeqtiggkf pyvfsecqai harsfipcqd tpsvkvpctf kirsklpvia sgipcgtanf
      181 cngsleylfe qknpipsylf cilsgdlast nigprssvyt epgnllacky efehdmenfm
      241 eaaeqltlpy cwtrydfvil ppsfpyggme npnatfatpt liagdrsnvn viahelahsw
      301 sgnlvtnesw qcfwlnegmt vflerkilgr lygeptrqfe aiigwgelee svkllgedse
      361 ytkliqnleg rdpddafstv pyekgsnfly eierviggps vfepflpfyf rkfakstvne
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      421 vkfkhalyey fsplglaskl dsidwdtwyh apgmppvkph fdttladpcy klaeswtnsa
      481 knsddpskfs skdienwsag qkslfldvvy eavsfphnyi krmgdvysfa esknaelsfr
      541 ffklalksky kplyntiaer vgsvgrmkfv rpifrllnea drafaietfe kykhfyhkic
      601 asqvekdlgl se
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☐ 1: CAA20138. Reports SPACUNK4.08 [Schi...[gi:3395554]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA20138                 793 aa            linear   PLN 16-APR-2005
DEFINITION  SPACUNK4.08 [Schizosaccharomyces pombe].
ACCESSION   CAA20138
VERSION     CAA20138.1  GI:3395554
DBSOURCE    embl accession AL031180.3
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 793)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
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            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
            Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
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            Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
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Cerutti L]]

COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers

source 1..793
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="I"
/map="IL"
/clone="cosmid c2E11 -chimeric"

Protein 1..793
/EC_number="3.4.14.-"
/name="SPACUNK4.08"

Region 125..494
/region_name="DPPIV_N"
/note="Dipeptidyl peptidase IV (DPP IV) N-terminal region. This family is an alignment of the region to the N-terminal side of the active site. The Prosite motif does not correspond to this Pfam entry; pfam00930"
/db_xref="CDD:64779"

Region 574..779
/region_name="Peptidase_S9"
/note="Prolyl oligopeptidase family; pfam00326"
/db_xref="CDD:64203"

CDS 1..793
/gene="SPACUNK4.08"
/coded_by="complement(AL031180.3:24320..26701)"
/note="dipeptidyl aminopeptidase (predicted); peptidase family S9; predicted N-terminal signal anchor; prolyl endopeptidase (predicted); similar to S. cerevisiae DAP2"
/db_xref="GOA:O14073"
/db_xref="InterPro:IPR001375"
/db_xref="InterPro:IPR002469"
/db_xref="InterPro:IPR002471"
/db_xref="UniProtKB/Swiss-Prot:O14073"

ORIGIN

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    121 sysisfdaky vlvsvnksqr wrhssfaqyy lyntetkdvn mlgqdnehwt islaewsptg
    181 hqlsfvynnd lyvrkndgnv qrltydgtvd vfngltdwiy eeevlsspst iwwspdsdki
    241 aflklnesei ptyhyplyta eldpslpefd ynkdmaikyp kpgnpnpsvs lfvadlnsna
    301 ssnfslwhne plaepvvqnv lwvntssvlv qftnrnstci tarlldtelk sihtvktecl
    361 eegwyevqqs akmfplnnsl vwenwsdgyf dilalddynh lafipfngss piyltsgawd
    421 vtdgpihidg dfgnvyflat lkdsterhly yvsldtleiy gitdngedeg yystsfspfg
    481 dfyvlnyhgp dvpwqelrst kdkdyclsle tnsrlkqqls sitlpsveyg kltfndttfn
    541 fmerrprnfd vnkkypvlff ayggpgsqqv aklfrvdfqa ylashpdfef ivvtldgrgt
    601 gfngnafrys vsrhlgewes ydqgqagkfw adlpfvdenh vgiwgwsygg yltlktletq
    661 dvfsygmava pvtdwrlyds vyterymdlp qynkegykns qihdyekfkq lkrffvahgt
```

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      781 idpstgvrqh rwd
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☐ 1: CAA19290. Reports SPBC4B4.10c [Schi...[gi:3169097]

BLink, Conserved Domains, Links

Comment Features Sequence

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LOCUS       CAA19290                 261 aa            linear   PLN 16-APR-2005
DEFINITION  SPBC4B4.10c [Schizosaccharomyces pombe].
ACCESSION   CAA19290
VERSION     CAA19290.1  GI:3169097
DBSOURCE    embl accession AL023706.1
KEYWORDS    .
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 261)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
            Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,
            Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
            Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,
            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
            Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,
            Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
            Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
            Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,
            Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
            Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
            Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
            Ussery,D., Barrell,B.G. and Nurse,P.
  TITLE     The genome sequence of Schizosaccharomyces pombe
  JOURNAL   Nature 415 (6874), 871-880 (2002)
   PUBMED   11859360
  REMARK    Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to
```

Cerutti L]]
REFERENCE 2 (residues 1 to 261)
AUTHORS Beck,A., Reinhardt,R., Lyne,M., Wood,V., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-1997) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and Max Planck Institut fuer Molekulare Genetik, Ihnestr. 73, D-14195 Berlin, Germany
COMMENT Notes:
Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.
(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers

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/clone="cosmid c4B4"

Protein 1..261
/name="SPBC4B4.10c"

Region 73..261
/region_name="APG5"
/note="Autophagy protein Apg5. Apg5 is directly required for the import of aminopeptidase I via the cytoplasm-to-vacuole targeting pathway; pfam04106"
/db_xref="CDD:67711"

CDS 1..261
/gene="SPBC4B4.10c"
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/note="apoptosis specific protein homolog; similar to S. cerevisiae APG5"
/db_xref="GOA:O74971"
/db_xref="InterPro:IPR007239"
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121 frtyffnclk esdyvrngss sgiialskae tdtywnailn hdyydfrpia ikilfskskf
181 iplkiylgan apiiqtsapl gsslgeflnk rlpdlfpscd kflivkpvih gitiflqsvl
241 delnrdfcyi dgflhivlmk v
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☐ 1: O74971. Reports Autophagy protein...[gi:62899674]


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LOCUS       O74971                  261 aa            linear   PLN 26-JUN-2007
DEFINITION  Autophagy protein 5 (Meiotically up-regulated gene 77 protein).
ACCESSION   O74971
VERSION     O74971  GI:62899674
DBSOURCE    swissprot: locus ATG5_SCHPO, accession O74971;
            class: standard.
            created: Apr 26, 2005.
            sequence updated: Nov 1, 1998.
            annotation updated: Jun 26, 2007.
            xrefs: AL023706.1, CAA19290.1, T40482
            xrefs (non-sequence databases): GeneDB_Spombe:SPBC4B4.10c,
            ArrayExpress:O74971, GO:0005829, GO:0005634, GO:0030437,
            InterPro:IPR007239, PANTHER:PTHR13040, Pfam:PF04106
KEYWORDS    Autophagy; Complete proteome; Meiosis; Nucleus; Protein transport;
            Transport; Ubl conjugation.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;
            Schizosaccharomycetes; Schizosaccharomycetales;
            Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE   1  (residues 1 to 261)
  AUTHORS   Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,
            Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,
            Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,
            Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,
            Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,
            Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,
            Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,
            Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,
            Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,
            Pearson,D., Quail,M.A., Rabbinowitsch,E., Rutherford,K., Rutter,S.,
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            Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
            Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,
            Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
            Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
            Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,
            Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
            Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,
            Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
            Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
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Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L., Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A., Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L., Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V., Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED 11859360

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=ATCC 38366 / 972
Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to Cerutti L]]

REFERENCE 2 (residues 1 to 261)

AUTHORS Martin-Castellanos,C., Blanco,M., Rozalen,A.E., Perez-Hidalgo,L., Garcia,A.I., Conde,F., Mata,J., Ellermeier,C., Davis,L., San-Segundo,P., Smith,G.R. and Moreno,S.

TITLE A large-scale screen in S. pombe identifies seven novel genes required for critical meiotic events

JOURNAL Curr. Biol. 15 (22), 2056-2062 (2005)

PUBMED 16303567

REMARK FUNCTION.

REFERENCE 3 (residues 1 to 261)

AUTHORS Matsuyama,A., Arai,R., Yashiroda,Y., Shirai,A., Kamata,A., Sekido,S., Kobayashi,Y., Hashimoto,A., Hamamoto,M., Hiraoka,Y., Horinouchi,S. and Yoshida,M.

TITLE ORFeome cloning and global analysis of protein localization in the fission yeast Schizosaccharomyces pombe

JOURNAL Nat. Biotechnol. 24 (7), 841-847 (2006)

PUBMED 16823372

REMARK SUBCELLULAR LOCATION [LARGE SCALE ANALYSIS].
Erratum:[Nat Biotechnol. 2006 Aug;24(8):1033]

COMMENT On Apr 26, 2005 this sequence version replaced gi:7490112.
[FUNCTION] Involved in cytoplasm to vacuole transport (Cvt) and autophagy vesicles formation. May be required for atg8 association to the vesicle membranes (By similarity). Has a role in meiosis.
[SUBCELLULAR LOCATION] Cytoplasm. Nucleus. Membrane; peripheral membrane protein (By similarity).
[PTM] Conjugated to atg12; which is essential for autophagy (By similarity).
[SIMILARITY] Belongs to the ATG5 family.

FEATURES Location/Qualifiers

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gene 1..261
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/note="synonym: mug77"

Protein 1..261
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/product="Autophagy protein 5"

Region 1..261
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/region_name="Mature chain"
/experiment="experimental evidence, no additional details recorded"
/note="Autophagy protein 5. /FTId=PRO_0000219008."

Region 73..261

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                     cytoplasm-to-vacuole targeting pathway; pfam04106"
                     /db_xref="CDD:67711"
     Bond            bond(148)
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                     /locus_tag="SPBC4B4.10c"
                     /bond_type="xlink"
                     /inference="non-experimental evidence, no additional
                     details recorded"
                     /note="Glycyl lysine isopeptide (Lys-Gly) (interchain with
                     G-Cter in ATG12) (By similarity)."
ORIGIN
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       61 ecwldyngvp lkwhwpvgll fdlltvfdpd tprapvlwri qlrsglfptt kilqmetmdt
      121 frtyffnclk esdyvrngss sgiialskae tdtywnailn hdyydfrpia ikilfskskf
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